

AMENDMENTS TO THE SPECIFICATION

Amend the paragraph beginning on page 32, line 18¹ of the original specification as follows:

The classification by Welinder et al. is based on the comparison of highly common sequences in the primary sequence of each peroxidase. In more detail, the classification is practiced by comparing the primary sequences around the His residue proximal to the heme iron and the His ~~and Arg residues~~ residue distal to the heme iron ~~and the Arg residue~~. Using the sequence comparison table prepared by Welinder et al., the DyP sequence was compared (Fig. 4). Herein, Fig. 4 includes CCP (Saccharomyces cerevisiae-derived cytochrome C peroxidase) and ECP (E. coli-derived peroxidase) as Class I peroxidases. Comparison was done with ARP (Arthromyces ramosus-derived peroxidase), MnP (manganic peroxidase derived from a fungus of the genus Phanerochaete) and LiP (Phanerochaete chrysosporium-derived lignin peroxidase) as Class II peroxidases. Additionally, Class III peroxidase includes TP (Tunip peroxidase) and HRP (horse radish peroxidase).

Amend the paragraph beginning on page 33, line 9² of the original specification as follows:

Because DyP is derived from the fungus, DyP is classified in Class II. However, it was shown that the ~~proximal~~ Arg residue (at the open square (□) position in the figure) characteristically found in Class II was absent and no homology was found with the sequence in the proximity of the distal His residue (at closed circle (●) position in the figure). This indicates that DyP as a fungus-derived peroxidase has a specific sequence.

¹ The only amendment to this paragraph appears at page 32, lines 22 and 23.

² The only amendment to this paragraph appears at page 33, line 10.